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L32: Entry 11 of 11 File: USPT Oct 19, 1999

DOCUMENT-IDENTIFIER: US 5968784 A
**** See image for Certificate of Correction ****
TITLE: Method for analyzing quantitative expression of genes

Brief Summary Text (11):
Other methods of determining peptide expression in an mRNA population involve the use of antibodies to probe populations of peptides produced from mRNA pools. Thus, "libraries" of synthetic polypeptides corresponding to the polypeptides coded for by mRNA molecules are produced and then probed by individual antibodies. This method does not provide for a detection of all of the polypeptides produced by the mRNA at one time as it may not detect low levels of expression. Moreover, the method is limited to available antibodies. This method is described in, for example, U.S. Pat. No. 5,242,798, issued Sep. 7, 1993, and in U.S. Pat. No. 4,900,811, issued Feb. 13, 1990.

Brief Summary Text (21):
The present invention provides a method for tagging and identifying all of the expressed genes in a given cell population. This method thus allows even mRNAs with low copy number to be detected. By comparing gene expression profiles among cells, this method may be used to identify individual genes whose expression is associated with a pathological phenotype. Using high throughput DNA sequencing and associated information system support to analyze such DNA sequencing, the method of the present invention also permits the generation of global gene expression profiles in a reasonable length and time. Thus, the present invention provides a simple and rapid method of obtaining sufficient data to use in an information system known to those of skill in the art to obtain global gene expression profile and identify genes of interest.

Brief Summary Text (95):
Another aspect of the present invention is a method for screening for the effects of a drug on a cell or tissue. The method of the present invention can be used to compare mRNA gene expression patterns in cells and tissues that have been treated with a drug versus cells and tissues that have not been treated with a drug. The cells or tissues may be from normal target organisms and the side effects of a drug may be tested, or the cells or tissues may be from diseased target organisms with particular disorders to determine whether the drug may change the gene expression profile in the diseased cells.

WEST Search History

DATE: Thursday, April 24, 2003

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,EPAB,DWPI; PLUR=YES; OP=ADJ			
L1	shoshan-a$.in. or wasserman-A$.in. or Mintz-E$.in. or mintz-L$.in. or faigler-S$.in.	83	L1
L2	transcriptome	25	L2
L3	RNA transcript	5245	L3
L4	alternativ$ spliced gene$1	15	L4
L5	penn-S$.in. or Rank-D$.in. or Hanzel-d$.in.	120	L5
L6	libar$3 and l2	0	L6
L7	l1 and l2	1	L7
L8	l1 and l4	0	L8
L9	L5 and l4	0	L9
L10	l5 and l3	0	L10
L11	RNA and l5	0	L11
L12	penn-Sharron$.in.	3	L12
L13	transcriptome	25	L13
L14	RNA transcript	5245	L14
L15	Alternativ$ spliced (genes or transcript or sequence)	227	L15
L16	(l13 or l14 or L15) and microarray	450	L16
L17	L16 and human	442	L17
L18	L17 and (plurality near (oligonucleotide or probe))	12	L18
L19	L17 and (high-throughput)	105	L19
L20	l19 and library	103	L20
L21	L18 and (messenger RNA or mRNA)	12	L21
L22	(plurality same (probe or oligonucleotide))	16738	L22
L23	L22 and l20	8	L23
L24	l2 and (microarray or array)	11	L24
L25	alternativ$ splic$ near (genes or sequence or transcript)	473	L25
L26	pool near RNA transcript	2	L26
L27	(plurality or pool) near (messenger RNA or mRNA)	280	L27
L28	L27 same microarray	4	L28
L29	L25 same microarry	0	L29
L30	L25 same microarray	1	L30
L31	l25 and gene expression profile	3	L31

L32	L27 and gene expression profile	11	L32
L33	RNA transcripts and differential display	210	L33
L34	L33 and l25	23	L34
L35	L34 and library	23	L35

END OF SEARCH HISTORY

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L32: Entry 3 of 11 File: USPT Jun 11, 2002

DOCUMENT-IDENTIFIER: US 6403316 B1
TITLE: Isolation of cDNA encoding for secreted or membranal proteins

Brief Summary Text (6):
Powerful bioinformatics tools have been developed in order to classify and identify interesting genes according to their gene expression profiles (Eisen et al,m 1998; Bassett et al., 1999) and associate them with a condition of interest. The identification and/or isolation of genes whose expression differs between two cell or tissue types, or between cells or tissues exposed to stress conditions, chemical compounds or pathogens, is critical to the understanding of mechanisms underlying various physiological conditions, disorders, or diseases. However, out of the many clones that are identified based on interesting expression patterns, only those representing known genes can be considered to be promising drugs or drug-targets. A significant portion of the differentially expressed, arrayed clones, are unknown ESTs frequently derived from untranslated cDNA regions or containing no informative structural protein patterns. Thus, no clues exist as to the potential function or sub-cellular localization of a large group of clones.

Detailed Description Text (9):
The method of the present invention synergistically integrates two types of previously known methodologies which were otherwise used separately. The first method is the division of cellular mRNA into separate pools of mRNA derived from different polysome pools. The second methodology involves the simultaneous comparison of the relative abundance of the mRNA species found in the separate pools by a method of differential analysis such as differential display (and its many variants), representational difference analysis (RDA), gene expression microarray (GEM), suppressive subtraction hybridization (SSH) (Diatchenko et al., 1996), and oligonucleotide chip techniques such as the chip technology exemplified by U.S. Pat. No. 5,545,531 to Rava et al. assigned to Affymax Technologies N.V. and direct sequencing exemplified by WO 96/17957 patent application to Hyseq, Inc.

Detailed Description Text (14):
Following isolation and division of the total mRNA population into separate protein localization pools of mRNA, the relative abundance of the many mRNA species found in these pools are simultaneously compared using a differential analysis technique such as differential display, oligonucleotide chips, representational difference analysis (RDA), GEM-Gene Expression Microarrays (Schena et al., 1995, Aiello et al., 1994, Shen et al., 1995, Bauer et al., 1993, Liang and Pardee, 1992, Liang and Pardee, 1995, Liang et al., 1993, Braun et al., 1995, Hubank and Schatz, 1994) and suppressive subtraction hybridization (SSH). The RNA isolated from the fractions can be further purified into mRNA without the ribosomal RNA by poly A selection. It should be noted that multiple pools can be analyzed utilizing this method. That is, different cell aliquots subjected to different stressors can be compared with each other as well as with the reference sample.

Detailed Description Text (46):
In order to elucidate the molecular mechanisms underlying physiological and pathological conditions, global gene expression profiles should be deconstructed and specific genes of interest identified. Among these, secreted and membranal proteins are natural prime targets both for drug development and for the investigation of physiological phenomena. This is due to the key role they play in initiating and orchestrating complex responses as well as to their accessibility for manipulation.

Profiling alternative splicing on fiber-optic arrays.

COMMENT: Comment in: Nat Biotechnol. 2002 Apr;20(4):346-7
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AB The human **transcriptome** is marked by extensive alternative mRNA splicing and the expression of many closely related genes, which may be difficult to distinguish using standard microarray techniques. Here we describe a sensitive and specific assay for parallel analysis of mRNA isoforms on a fiber-optic microarray platform. The method permits analysis of **mRNA transcripts** without prior RNA purification or cDNA synthesis. Using an endogenously expressed viral transcript as a model, we demonstrated that the assay readily detects mRNA isoforms from as little as 10-100 pg of total cellular RNA or directly from a few cells. Multiplexed analysis of human cancer cell lines revealed differences in mRNA splicing and suggested a potential autocrine mechanism in the development of choriocarcinomas. Our approach may be useful in the large-scale analysis of the role of alternative splicing in development and disease.